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OIKE

RAW SEQUENCE LISTING

DATE: 09/18/2001

PATENT APPLICATION: US/09/942,374

TIME: 11:31:26

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\09182001\I942374.raw

4 <110> APPLICANT: Glucksmann, Maria Alexsandra
 5 Gimeno, Ruth
 6 White, David
 8 <120> TITLE OF INVENTION: 57242, a Human G-Protein Coupled
 9 Receptor Family Member and Uses Therefor
 12 <130> FILE REFERENCE: MPI2000-368P1R
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/942,374
 C--> 14 <141> CURRENT FILING DATE: 2001-08-29
 14 <150> PRIOR APPLICATION NUMBER: US 60/228,409
 15 <151> PRIOR FILING DATE: 2000-08-29
 17 <160> NUMBER OF SEQ ID NOS: 9
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1194
 23 <212> TYPE: DNA
 24 <213> ORGANISM: human
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (154)...(1194)
 30 <400> SEQUENCE: 1

31 gcaccagcca acccacacac acaggacccg catcctgggt gatgaagtca gacacrcagc 60
 32 agctgggtga gtgctaacgc tcagataagc atctgtgcc ttgtggggac tccctgggct 120
 33 gctctgcacc cggacacctg ctctgtcccc gcc atg tac aac ggg tcg tgc tgc 174
 34 Met Tyr Asn Gly Ser Cys Cys
 35 1 5
 37 cgc atc gag ggg gac acc atc tcc cag gtg atg ccg ccg ctg ctc att 222
 38 Arg Ile Glu Gly Asp Thr Ile Ser Gln Val Met Pro Pro Leu Leu Ile
 39 10 15 20
 41 gtg gcc ttt gtg ctg ggc gca cta ggc aat ggg gtc gcc ctg tgt ggt 270
 42 Val Ala Phe Val Leu Gly Ala Leu Gly Asn Gly Val Ala Leu Cys Gly
 43 25 30 35
 45 ttc tgc ttc cac atg aag acc tgg aag ccc agc act gtt tac ctt ttc 318
 46 Phe Cys Phe His Met Lys Thr Trp Lys Pro Ser Thr Val Tyr Leu Phe
 47 40 45 50 55
 49 aat ttg gcc gtg gct gat ttc ctc ctt atg atc tgc ctg cct ttt cgg 366
 50 Asn Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu Pro Phe Arg
 51 60 65 70
 53 aca gac tat tac ctc aga cgt aga cac tgg gct ttt ggg gac att ccc 414
 54 Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ala Phe Gly Asp Ile Pro
 55 75 80 85
 57 tgc cga gtg ggg ctc ttc acg ttg gcc atg aac agg gcc ggg agc atc 462
 58 Cys Arg Val Gly Leu Phe Thr Leu Ala Met Asn Arg Ala Gly Ser Ile
 59 90 95 100
 61 gtg ttc ctt acg gtg gtg gct gcg gac agg tat ttc aaa gtg gtc cac 510
 62 Val Phe Leu Thr Val Val Ala Ala Asp Arg Tyr Phe Lys Val Val His
 63 105 110 115
 65 ccc cac cac gcg gtg aac act atc tcc acc ccg gtg gcg gct ggc atc 558

ENTERED

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66 Pro His His Ala Val Asn Thr Ile Ser Thr Arg Val Ala Ala Gly Ile
67 120                125                130                135
69 gtc tgc acc ctg tgg gcc ctg gtc atc ctg gga aca gtg tat ctt ttg 606
70 Val Cys Thr Leu Trp Ala Leu Val Ile Leu Gly Thr Val Tyr Leu Leu
71                140                145                150
73 ctg gag aac cat ctc tgc gtg caa gag acg gcc gtc tcc tgt gag agc 654
74 Leu Glu Asn His Leu Cys Val Gln Glu Thr Ala Val Ser Cys Glu Ser
75                155                160                165
77 ttc atc atg gag tgc gcc aat ggc tgg cac gac atc atg ttc cag ctg 702
78 Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met Phe Gln Leu
79                170                175                180
81 gag ttc ttt atg ccc ctc ggc atc atc tta ttt tgc tcc ttc aag att 750
82 Glu Phe Phe Met Pro Leu Gly Ile Ile Leu Phe Cys Ser Phe Lys Ile
83                185                190                195
85 gtt tgg agc ctg agg cgg agg cag cag ctg gcc aga cag gct cgg atg 798
86 Val Trp Ser Leu Arg Arg Arg Gln Gln Leu Ala Arg Gln Ala Arg Met
87 200                205                210                215
89 aag aag gcg acc cgg ttc atc atg gtg gtg gca att gtg ttc atc aca 846
90 Lys Lys Ala Thr Arg Phe Ile Met Val Val Ala Ile Val Phe Ile Thr
91                220                225                230
93 tgc tac ctg ccc agc gtg tct gct aga ctc tat ttc ctc tgg acg gtg 894
94 Cys Tyr Leu Pro Ser Val Ser Ala Arg Leu Tyr Phe Leu Trp Thr Val
95                235                240                245
97 ccc tcg agt gcc tgc gat ccc tct gtc cat ggg gcc ctg cac ata acc 942
98 Pro Ser Ser Ala Cys Asp Pro Ser Val His Gly Ala Leu His Ile Thr
99                250                255                260
101 ctc agc ttc acc tac atg aac agc atg ctg gat ccc ctg gtg tat tat 990
102 Leu Ser Phe Thr Tyr Met Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr
103                265                270                275
105 ttt tca agc ccc tcc ttt ccc aaa ttc tac aac aag ctc aaa atc tgc 1038
106 Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Asn Lys Leu Lys Ile Cys
107 280                285                290                295
109 agt ctg aaa ccc aag cag cca gga cac tca aaa aca caa agg ccg gaa 1086
110 Ser Leu Lys Pro Lys Gln Pro Gly His Ser Lys Thr Gln Arg Pro Glu
111                300                305                310
113 gag atg cca att tcg aac ctc ggt cgc agg agt tgc atc agt gtg gca 1134
114 Glu Met Pro Ile Ser Asn Leu Gly Arg Arg Ser Cys Ile Ser Val Ala
115                315                320                325
117 aat agt ttc caa agc cag tct gat ggg caa tgg gat ccc cac att gtt 1182
118 Asn Ser Phe Gln Ser Gln Ser Asp Gly Gln Trp Asp Pro His Ile Val
119                330                335                340
121 gag tgg cac tga 1194
122 Glu Trp His *
123                345
126 <210> SEQ ID NO: 2
127 <211> LENGTH: 346
128 <212> TYPE: PRT
129 <213> ORGANISM: human
131 <400> SEQUENCE: 2

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132 Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
133 1 5 10 15
134 Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
135 20 25 30
136 Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
137 35 40 45
138 Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
139 50 55 60
140 Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
141 65 70 75 80
142 Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
143 85 90 95
144 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
145 100 105 110
146 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
147 115 120 125
148 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
149 130 135 140
150 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
151 145 150 155 160
152 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
153 165 170 175
154 His Asp Ile Met Phe Gln Leu Glu Phe Met Pro Leu Gly Ile Ile
155 180 185 190
156 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
157 195 200 205
158 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
159 210 215 220
160 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
161 225 230 235 240
162 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
163 245 250 255
164 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
165 260 265 270
166 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
167 275 280 285
168 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
169 290 295 300
170 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
171 305 310 315 320
172 Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly
173 325 330 335
174 Gln Trp Asp Pro His Ile Val Glu Trp His
175 340 345
178 <210> SEQ ID NO: 3
179 <211> LENGTH: 1041
180 <212> TYPE: DNA
181 <213> ORGANISM: human
183 <400> SEQUENCE: 3

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```

184 atgtacaacg ggtcgtgctg ccgcatcgag ggggacacca tctcccaggt gatgccgccg 60
185 ctgctcattg tggcctttgt gctgggcgca ctaggcaatg gggtcgccct gtgtgggtttc 120
186 tgcttccaca tgaagacctg gaagcccagc actgtttacc ttttcaattt ggccgtgggt 180
187 gatttcctcc ttatgatctg cctgcctttt cggacagact attacctcag acgtagacac 240
188 tgggcttttg gggacattcc ctgcccagtg gggctcttca cgttggccat gaacagggcc 300
189 gggagcatcg tgttccttac ggtgggtggc gcggacaggt atttcaaagt ggtccacccc 360
190 caccacgcgg tgaacactat ctccaccccg gtggcggtcg gcatcgtctg caccctgtgg 420
191 gccctggcca tcctgggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag 480
192 acggccgtct cctgtgagag cttcatcatg gagtcggcca atggctggca cgacatcatg 540
193 ttccagctgg agttctttat gccctcggc atcatcttat ttgctcctt caagattggt 600
194 tggagcctga ggcggaggca gcagctggcc agacaggctc ggatgaagaa ggcgacccgg 660
195 ttcatcatgg tgggtggcaat tgtgttcac acatgctacc tgcccagcgt gtctgctaga 720
196 ctctatttcc tctggacggt gccctcgagt gcctgcgac cctctgtcca tggggccctg 780
197 cacataaccc tcagcttcac ctacatgaac agcatgctgg atccccctgt gtattatttt 840
198 tcaagccctt cctttcccaa attctacaac aagctcaaaa tctgcagtct gaaacccaag 900
199 cagccaggac actcaaaaac acaaaggccg gaagagatgc caatttcgaa cctcggtcgc 960
200 aggagttgca tcagtgtggc aaatagtttc caaagccagt ctgatgggca atgggatccc 1020
201 cacattgttg agtggcactg a
1041
203 <210> SEQ ID NO: 4
204 <211> LENGTH: 19
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: murine 57242 primer sequence
211 <400> SEQUENCE: 4
212 ggcagcagct gaccagaca
19
214 <210> SEQ ID NO: 5
215 <211> LENGTH: 21
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: murine 57242 primer sequence
222 <400> SEQUENCE: 5
223 gaacacagaa gccaccacca t
21
225 <210> SEQ ID NO: 6
226 <211> LENGTH: 23
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: murine 57242 probe sequence
233 <400> SEQUENCE: 6
234 atgaggaggg ccaccgggt cat
23
236 <210> SEQ ID NO: 7
237 <211> LENGTH: 20
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: human 57242 primer sequence
244 <400> SEQUENCE: 7

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245 tgcagtctga aacccaagca 20
247 <210> SEQ ID NO: 8
248 <211> LENGTH: 17
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: human 57242 primer sequence ✓
255 <400> SEQUENCE: 8
256 tgcgaccgag gttcgaa 17
258 <210> SEQ ID NO: 9
259 <211> LENGTH: 23
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: human 57242 probe sequence ✓
266 <400> SEQUENCE: 9
267 cacaaaggcc ggaagagatg cca 23
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VERIFICATION SUMMARY

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PATENT APPLICATION: US/09/942,374

TIME: 11:31:27

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\09182001\I942374.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date